

Claims

We claim:

1 *DNA 1* 1. A polynucleotide encoding a mutant starch biosynthesis protein, or a biologically-active fragment or variant of said mutant protein, wherein said mutant protein exhibits increased heat stability relative to the wild type protein.

1 2. The polynucleotide according to claim 1, wherein said mutant protein encoded by  
2 said polynucleotide is a plant AGP protein.

1 *DNA 2* 3. The polynucleotide according to claim 2, wherein said mutant protein encoded by  
2 said polynucleotide comprises an amino acid mutation in the large subunit of said protein.

1 4. The polynucleotide according to claim 2, wherein said mutant protein encoded by  
2 said polynucleotide comprises an amino acid mutation in the small subunit of said protein.

1 5. The polynucleotide according to claim 3, wherein said mutant protein encoded by  
2 said polynucleotide comprises an amino acid mutation wherein a histidine residue at position  
3 333 in the amino acid sequence of said protein is replaced by an amino acid that confers heat  
4 stability to said protein.

1 6. The polynucleotide according to claim 5, wherein said amino acid substituted for  
2 histidine at position number 333 is a glycine.

1 7. The polynucleotide according to claim 5, wherein said amino acid substituted for  
2 histidine at position number 333 is a phenylalanine.

1           8. The polynucleotide according to claim 5, wherein said amino acid substituted for  
2           histidine at position number 333 is a methionine.

1           9. The polynucleotide according to claim 1, wherein said mutant protein encoded by  
2           said polynucleotide further comprises an amino acid mutation that confers increased seed  
3           weight to a plant expressing said polynucleotide.

1           10. The polynucleotide according to claim 9, wherein said polynucleotide comprises  
2           the *Rev6* mutation.

1           11. The polynucleotide according to claim 9, wherein said polynucleotide encodes  
2           a maize large subunit AGP enzyme wherein at least one serine residue is inserted between  
3           amino acids 494 and 495 of the native AGP enzyme subunit.

1           12. The polynucleotide according to claim 9, wherein said polynucleotide encodes  
2           a maize large subunit AGP enzyme wherein the amino acid pair tyrosine:serine is inserted  
3           between amino acids 494 and 495 of the native AGP enzyme subunit.

1           13. The polynucleotide according to claim 9, wherein said polynucleotide encodes  
2           a maize large subunit AGP enzyme wherein the amino acid pair serine:tyrosine is inserted  
3           between amino acids 495 and 496 of the native AGP enzyme subunit.

1           14. A method for increasing resistance of a plant to heat stress conditions, said  
2           method comprising incorporating the polynucleotide of claim 1 into the genome of said plant  
3           and expressing the protein encoded by said polynucleotide molecule.

1           15. The method according to claim 14, wherein said plant is a monocotyledonous  
2           plant.

1           16. The method according to claim 15, wherein said monocotyledonous plant is  
2 selected from the group consisting of rice, wheat, barley, oats, sorghum, maize, lilies, and  
3 millet.

1           17. The method according to claim 14, wherein said plant is *Zea mays*.

1           18. The method according to claim 14, wherein said plant is a dicotyledonous plant.

1           19. The method according to claim 18, wherein said dicotyledonous plant is selected  
2 from the group consisting of peas, alfalfa, chickpea, chicory, clover, kale, lentil, prairie grass,  
3 soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple trees, and lettuce.

1           20. A plant or plant tissue comprising the polynucleotide molecule of claim 1.

1           21. The plant or plant tissue according to claim 20, wherein said plant or plant tissue  
2 is monocotyledonous.

1           22. The plant or plant tissue according to claim 21, wherein said monocotyledonous  
2 plant or plant tissue is selected from the group consisting of rice, wheat, barley, oats,  
3 sorghum, maize, lilies, and millet.

1           23. The plant or plant tissue according to claim 20, wherein said plant is *Zea mays*  
2 or said plant tissue is from *Zea mays*.

1           24. The plant or plant tissue according to claim 20, wherein said plant or plant tissue  
2 is dicotyledonous.

1           25. The plant or plant tissue according to claim 24, wherein said dicotyledonous plant  
2           or plant tissue is selected from the group consisting of peas, alfalfa, chickpea, chicory, clover,  
3           kale, lentil, prairie grass, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple  
4           trees, and lettuce.

1           26. The plant tissue according to claim 20, wherein said plant tissue is a seed.

1 *W<sup>o</sup>s >* 27. A mutant starch biosynthesis protein encoded by the polynucleotide of claim 1.

1           28. A method for identifying a polynucleotide encoding a mutant starch biosynthesis  
2           protein wherein said mutant starch biosynthesis protein exhibits increased heat stability  
3           relative to a wild type protein, said method comprising mutating a polynucleotide encoding  
4           a starch biosynthesis protein, expressing said mutated polynucleotide in a cell to produce a  
5           mutant starch biosynthesis protein, and determining whether said mutant starch biosynthesis  
6           protein exhibits increased heat stability relative to the wild type starch biosynthesis protein.

1           29. A method for increasing a characteristic of a plant selected from the group  
2           consisting of seed number, plant biomass, Harvest Index, flag leaf weight, seed heads, and  
3           total seed weight, said method comprising incorporating the polynucleotide of claim 10 into  
4           the genome of said plant and expressing the protein encoded by said polynucleotide molecule.